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Abstract

A method of analyzing a sequence of a polynucleotide of interest, comprising the steps of: a) incorporating one member of a specific binding pair at the end of each strand of a double stranded polynucleotide of interest, the number being of the same type for both strands, b) immobilizing both strands of the polynucleotide to a solid support provided with the other member of the specific binding pair, c) annealing sequencing primers to the immobilized strands, d) sequencing both strands by the chain termination method. The polynucleotide of interest is preferably amplified before or in connection with step a) and most preferably by polymerase chain reaction extension. The invention also comprises a kit for use in analyzing the sequence of a polynucleotide of interest.

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